

# ERRATA

## Moloney Murine Leukemia Virus Envelope Protein Subunits, gp70 and Pr15E, Form a Stable Disulfide-Linked Complex

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Volume 72, no. 8, p. 6537–6545, 1998. Page 6540, Fig. 3C should appear as shown below.

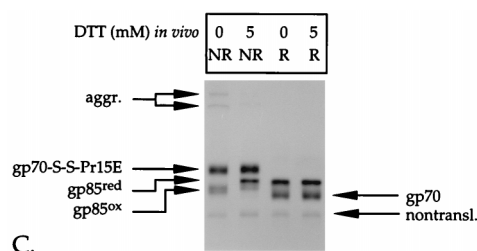


FIG. 3C.

## The Second Extracellular Loop of CXCR4 Determines Its Function as a Receptor for Feline Immunodeficiency Virus

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Volume 72, no. 8, p. 6475–6481, 1998. Page 6475, column 2, line 16: “C” should read “R;” line 17, “C5” should read “R5.”

## DNA Vaccination Affords Significant Protection against Feline Immunodeficiency Virus Infection without Inducing Detectable Antiviral Antibodies

MARGARET J. HOSIE, J. NORMAN FLYNN, MARK A. RIGBY, CELIA CANNON, THOMAS DUNSFORD, NANCY A. MACKAY, DAVID ARGYLE, BRIAN J. WILLETT, TAKAYUKI MIYAZAWA, DAVID E. ONIONS, OSWALD JARRETT, AND JAMES C. NEIL

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Volume 72, no. 9, p. 7310–7319, 1998. Page 7316, Table 1, line 1 of data: Trial 1, FIVΔRT, 12-week postchallenge response, “–, 0, blank” should read “+, –, 0.”

# Functional Interaction of Human Immunodeficiency Virus Type 1 Vpu and Gag with a Novel Member of the Tetratricopeptide Repeat Protein Family

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Volume 72, no. 6, p. 5189–5197, 1998. Page 5192: We found that nucleotide 932 (G) was omitted from the originally published *ubp* sequence. This resulted in changes in all the encoded amino acids following this position. The *ubp* cDNA is 2,222 bp long, with a 942-bp open reading frame and a 1,242-bp 3' untranslated region. The *ubp* open reading frame is predicted to encode a 313-residue protein with a molecular mass of 34.1 kDa, which is consistent with the mobility of UBP on polyacrylamide gels. These changes do not alter the conclusions made in the original publication. Figure 1 should appear as shown below.

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1   TCGGTCGCCTGAGAGGTATCACCTCTTCTGGGCTCAAGATGGACAACAAGAGCGCTGGCCTACGCCATCATCCAGTTCTTCGCATGACCAGCTCCGGCA
      M D N K K R L A Y A I I Q F L H D Q L R H>
101 CGGGGGCCTCTCGTCCGATGCTCAGGAGAGCTTGAAGTCCGCATCCAGTGCTGGAGACTGCGTTTGGGGTGACGGTAGAAGACAGTGACCTTGGCGTC
      G G L S S D A Q E S L E V A I O C L E T A F G V T V E D S D L A L >
201 CCTCAGACTCTGCCGGAGATATTTGAAGCGGCTGCCACGGGCAAGGAGATGCCCGAGGACCTGAGGAGCCAGCGCGAACCCCGCTTCCGAGGAGGACT
      P Q T L P E I F E A A A T G K E M P Q D L R S P A R T P P S E E D S>
301 CAGCAGAGGCAGAGCGCTCAAAACCGAAGAAACGAGCAGATGAAAGTGGAAAACCTTTGAAGCTGCCGTGCATTTCTACGGAAGCCATCGAGCTCAA
      A E A E R L K T E G N E O M K V E N F E A A V H F Y G K A I E L N>
401 CCCAGCCAACGCGCTCTATTTCTGCAACAGAGCCGACGCTACAGCAAACTCGGCAACTACGAGGCGCGGTGACGAGCTGTGAGCGGGCCATCTGCATT
      P A N A V Y F C N R A A A Y S K L G N Y A G A V Q D C E R A I C I>
501 GACCCGGCTTACAGCAAGGCTTACGGCAGGATGGGCTTGGCGCTCTCCAGCCTCAACAAGCACGTGGAGGCGGTGGCTTACTACAAGAAGGCGCTGGAGC
      D P A Y S K A Y G R M G L A L S S L N K H V E A V A Y Y K K A L E L>
601 TGGACCCGACAACGAGACATACAAGTCCAACCTCAAGATAGCGGAGCTGAAGCTGCGGGAGGCCCCAGCCCCAGGGAGGCGTGGGCGAGCTTCGACAT
      D P D N E T Y K S N L K I A E L K L R E A P S P T G G V G S F D I>
701 CGCCGGCTGCTGAACAACCTTGGCTTCATGAGCATGGCTTCGAACCTAATGAACAATCCCAGATTACAGAGCTCATGTCCGGCATGATTTCCGGTGGC
      A G L L N N P G F M S M A S N L M N N P Q I Q Q L M S G M I S G G>
801 AACAAACCCCTGGGAACCTCCCGCACCGCCCTCGCAGAACGACCTGGCCAGCCTCATCCAGGCGGGCCAGCAGTTTCCAGCAGATGCAGCAGCAGA
      N N P L G T P G T S P S Q N D L A S L I Q A G Q Q F A Q Q M Q Q Q N>
901 ACCCAGAGTTGATAGAGCAGCTCAGGAGCCAGATCCGGAGTCGGACGCGCCAGCGCCAGCAACGACGACCAGCAGGAGTGACGCTGCCTGCCCTCCCGTGTG
      P E L I E Q L R S Q I R S R T P S A S N D D Q Q E *
1001 ACCGCGTCTTCCCTGGCGACCCGAAGGAGCCTTCTGGTTGCTGCCACTTCCTCTGTGGACTGCTCGTAGAGAGGGGAAGAGAGACCTCGGACC
1101 TGCATGTCAAGATGGATTTTCCCTTTTATCTCTGCCCTCCTCCACTCCCTTTTGTAACTCCCTTACAGCCCCAGACCTTCTTGAACGAGAGCCAG
1201 CAAGCTGAGCACAGACCAGCAGCGACCTCCCTTCCAGCCCCAGAAAGCTCGGTCACTTGAGTGTTTTCTAGAATCTTGGGTGCTCCCGGGCCGCTCTC
1301 AGAGAACTGGCAGGTTTACAGTTCAGCCGTGTGGCGGATCGTGTGGCTTCCAAAGCCCTTTACAGCCCCGCCGCCCATCCCGTGGTCTGTCTGCAGGAA
1401 CTCTCCCGCTGTGTGAGAAAGCCTTTCCGAGTCGACCTCCCGGCCACCCCGGCCCTGTGCCTGCTCGGAAGAGCTCACTGCCAGCTGCGGCCCTGGGCAAC
1501 GCGGGCCATGTGTGTTGATGAGGAACTCTTTAGTGGCAGACACCTAAGAGACGGCTGCGGTACCCACGCTCCGTGGCTCAGGAGCCGTCTGGGT
1601 GCATAGGACCACTTTCTGTGACTTTTCTCCAGTTGGGATGTTGACAGACATGTTTCCCTCCTCCACCTCATTTTCTGGTCCCTCGCAGCTGAGAGCC
1701 AGGGCCGACATCATGACCTTCTGTCCCGGCCGCTTAGCCCGGGAACAGGGAAGGAGCTGGGCCGTTTCTGTCTGTGTCCTATCCTGCTGCTCTCTG
1801 TCCTGGATGTTTTCATGGGCCCCGGGCCCCAGGGAAGCTTACCCCTCCTGTGCTGGGTGGAGGCCACGGACACCTCAGGTGCCACCCACTTGGCCCT
1901 AAAACAGCCACAGGAAAGCAGCCGAGAGCCGACAGCGGGCAGCCTGTCTGGGTTCTGAGGCTGGGGGTGGCAGACGAACCCACGGCGCCGTGGTC
2001 CCAGCAGCAGGTTGTGTCAGTCGAGCATCTTGGGCTCCCTGGCTCCTGGCGCTGTGTAGGTAGGNGCAGTACCGTGTATCGTAGGTAGCAGTAGGAAC
2101 GGGGGCCACCGCGGCCCTGCAGCCGTTCATGGCGGTGAGGTGTGTGCCAAGCCCAACCGGGGTGCAGGGCGTGACGTGTGGGGAATAAATAGCGTTGTG
2201 ACCTCAAAAAAAAAAAAAAAAAA

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FIG. 1.